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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/077,130	02/15/2002	Rosana Kapeller-Libermann	MPI01-047P1RNM	2926

7590 10/25/2004  
Jean M. Silveri  
Millennium Pharmaceuticals, Inc.  
75 Sidney Street  
Cambridge, MA 02139

EXAMINER

MONSHIPOURI, MARYAM

ART UNIT	PAPER NUMBER
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1652

DATE MAILED: 10/25/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

## Office Action Summary

**Application No.**

10/077,130

**Applicant(s)**

KAPELLER-LIBERMANN ET AL.

**Examiner**

Maryam Monshipouri

**Art Unit**

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☐ Responsive to communication(s) filed on \_\_\_\_.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 1-22 is/are pending in the application.
- 4a) Of the above claim(s) 8-11, 13-17 and 19-22 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-7, 12 and 18 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- ☒ Notice of References Cited (PTO-892)
- ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)  
Paper No(s)/Mail Date filed 7/30/04
- ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_
- ☐ Notice of Informal Patent Application (PTO-152)
- ☒ Other: attachment

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Applicant's response to restriction letter filed 7/30/2004 is acknowledged.

Applicant elected Group II invention directed to claims 1-7, 12 and 18 and SEQ ID NO:5 encoding sequences only, without traverse. Claims 8-11, 13-17 and 19-22 are withdrawn as drawn to non-elected invention.

### **DETAILED ACTION**

Claims 1-7, 12 and 18 (directed to sequences encoding SEQ ID NO:5 only) are under examination on the merits.

#### ***Claim Objections***

Claims 1-7, 12 and 18 are objected to because of the following informalities: said claims recite both elected (SEQ ID NO:4 and 6) as well as non-elected sequences (SEQ ID NO: 1 and 3). Applicant is advised to delete the non-elected sequences from the elected claims. Appropriate correction is required.

#### ***Claim Rejections - 35 USC § 112***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-7, 12 and 18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The term "stringent conditions" in claim 1 (and its dependent claims 2-7 and 18), and claim 12 is unclear. Applicant has not defined this term explicitly, in the specification. In page 17 of the disclosure, many examples of stringent conditions are recited but the exact salt and temperature conditions that correspond to said term are not identified. Applicant may overcome this rejection by

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recitation of exact salt and temperature conditions used for hybridization (based in the support provided in the specification) into claims 1 and 12. Currently claims 2-7 are merely rejected for depending from a rejected base claim.

Claims 1-7, 12 and 18 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The term "naturally occurring allelic variant" in claim 1 (and its dependent claims 2-7 and 18) and claim 12 is unclear. Applicant in pages 26-27 of the disclosure has provided a definition for said term but said definition is unclear. For example, in page 26 of the disclosure applicant defines allelic variants as both functional and non-functional. The functional variants according to applicant, must have only conservative substitution of one or more amino acids of SEQ ID NO:5 in non-critical regions of SEQ ID NO:5. However, it is not clear what number constitutes the term "more" and what region constitutes "non-critical". The latter term remains puzzling in defining non-functional variants as well.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-7, 12 and 18 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for isolated DNA sequences encoding SEQ ID NO:5, does not reasonably provide enablement for any of the following:

- isolated DNA molecules comprising DNA sequences which are at least 85% identical to SEQ ID NO:4 and 6 with no function (see base claims 1 and 12),

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- Isolated DNA molecules comprising a fragment of at least 300 nucleotides of SEQ ID NO:4 and 6 with no function,
- Isolated DNA molecules encoding a fragment comprising at least 15 contiguous amino acids of SEQ ID NO :5 with no function, and
- Isolated DNA molecules encoding a naturally occurring allelic variant of SEQ ID NO:5, wherein the nucleic acid molecules hybridize to SEQ ID NO:4 or 6 or complements thereof, under stringent conditions, with no function.

The specification fails to teach which residues in the above listed DNA molecules must be retained such that said DNA molecules encode products with kinase function. No examples of such sequences are provided either. Current state of the art indicates that any DNA sequence that: (a) has 85% identity, (b) comprises 300 nucleotides of a sequence encoding a full-length polypeptide or encodes (c) a fragment of at least 15 amino acids of a full-length polypeptide or (d ) a naturally occurring allelic variant of said full-length polypeptide is not necessarily going to encode a product with kinase activity.

Therefore due to lack of sufficient teachings and examples provided in the specification and due to unpredictability of prior art as to which residues in above mentioned DNA sequences must be retained such that said DNA sequences encode products that have kinase function one of skill in the art has to go through the burden of undue experimentation in order to screen for those sequences that are supported by the specification and as such claims 1 and 12 go beyond the scope of the disclosure. Claims 2-7 and 18 are rejected merely for depending from rejected base claim 1.

Claims 1, 2-7, 12 and 18 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Claims 1 (and its dependent claims 3-7) and 12 are directed to **genera** of DNA sequences that are not adequately described in the specification.

These claims are directed to the following genera:

- A genus of DNA molecules comprising DNA sequences which are at least 85% identical to SEQ ID NO:4 and 6 with no function (see base claims 1 and 12).
- A genus of DNA molecules comprising a fragment of at least 300 nucleotides of SEQ ID NO:4 and 6 with no function.
- A genus of DNA molecules encoding a fragment comprising at least 15 contiguous amino acids of SEQ ID NO :5 with no function.
- A genus of DNA molecules encoding a naturally occurring allelic variant of SEQ ID NO:5, wherein the nucleic acid molecules hybridize to SEQ ID NO:4 or 6 or complements thereof under stringent conditions, with no function.

The specification does not contain any disclosure of the function of all DNA sequences that are listed above. The genera of cDNAs that comprise these above cDNA molecules is a large variable genera with the potentiality of encoding many

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different proteins. Therefore, many functionally unrelated DNAs are encompassed within the scope of these claims, including partial DNA sequences. The specification discloses only **a single species** (DNA sequences encoding SEQ ID NO:5) for each claimed genus which is insufficient to put one of skill in the art in possession of the attributes and features of all species within the claimed genus. Therefore, one skilled in the art cannot reasonably conclude that the applicant had possession of the claimed invention at the time the instant application was filed.

Applicant is further reminded that the above listed genera are further subject to written description rejection because of lack of adequate structural information. For example, the specification does not provide enough information about the DNA sequences that have 85% identity to SEQ ID NO:4 or 6. In other words the specification does not teach which residues in which region of SEQ ID NO:4 and 6 may be mutated such that they are still capable of encoding products with kinase function. Similarly, in claim 1 (b) and (d) and claim 12 (b) the disclosure is silent as to what the other residues of claimed DNA sequences must be such that said DNA sequences can still encode products with kinase function. With respect to naturally occurring allelic variants in claim 1(e) and 12 (c ) again the lack of structural information persists. This is because as explained above, the definition of allelic variants in terms of structure is unclear. Thus, by reading the information provided about the genus of "allelic variants" in the disclosure one of skill in the art finds neither adequate structural nor adequate functional information (see specially non-functional variants), rendering claim 1 (and its dependent claims 3-7 and 18) and claim 12 even more subject to 112 first rejection.

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Applicant is referred to the revised interim guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at [www.uspto.gov](http://www.uspto.gov).

***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1, 3-7, 12 and 18 are rejected under 35 U.S.C. 102(e) as being anticipated by Wei et al. (U.S. Patent No. 6,482,624, issued Nov. 2002, cited in the IDS). Wei teaches a DNA sequence (see its SEQ ID NO:1) that encodes a polypeptide comprising at least 15 contiguous amino acids of SEQ ID NO:5 (see the attached amino acid alignment for residues matching residues 6356-7135 of SEQ ID NO:5). Wei also teaches (see columns 24-25) and claims vectors and hosts comprising its DNA sequences and methods of expressing its DNA sequence, anticipating claims 3-7 and 12. In column 29, Wei teaches about kits comprising its DNA sequences for detecting a kinase encoding nucleic acids in a biological sample, anticipating claim 18.

Claims 1, 3-7, 12 and 18 are rejected under 35 U.S.C. 102(e) as being anticipated by Zeng et al. (US20030108533 June 2003). Zeng teaches about a DNA sequence (see its SEQ ID NO:5) that encodes a polypeptide comprising at least 15



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contiguous amino acids of SEQ ID NO:5 of this invention (see the attached amino acid alignment for residues matching residues 5373-7968 of SEQ ID NO:5). Zeng also teaches (see page 2, column 1) and claims vectors and hosts comprising its DNA sequences and methods of expressing its DNA sequence anticipating claims 3-7 and 12. In page 2, column 2, Zeng teaches about kits comprising its DNA sequences for detecting a kinase encoding nucleic acids in a biological sample, anticipating claim 18.

**No claims are allowed.**

**ALLOWABLE SUBJECT MATTER**

**Isolated DNA sequences encoding SEQ ID NO:5 or comprising SEQ ID NO:4 or 6 are free of prior art. Further, the prior art does not teach or suggest preparing such specific sequences.**

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Maryam Monshipouri whose telephone number is (571) 272-0932. The examiner can normally be reached on 7:00 a.m to 4:30 p.m. except for alternate Mondays.

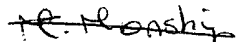
If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnanthapu Achutamurthy can be reached on (571) 272-0928. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR.

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Status information for unpublished applications is available through Private PAIR only.

For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



Maryam Monshipouri Ph.D.

Primary Examiner

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QY 6779 ARHLCDTGGSSSSSDNELAPARAKSLPPSVTHSPILLHPRGFLRPPASLPBAAEA 6838  
DB 1441 ARHLCDTGGSSSSSDNELAPARAKSLPPSVTHSPILLHPRGFLRPPASLPBAAEA 1500  
QY 6839 SERSTEAPAPPAGAGPAPAGCGVPRHSVIRSLFYHQAGESPESHGALAPGSRHRHPARR 6898  
DB 1501 SERSTEAPAPPAGAGPAPAGCGVPRHSVIRSLFYHQAGESPESHGALAPGSRHRHPARR 1560  
QY 6899 RHLLKGGYTAGALPGLRPLMEHRVLEPEABEECATLLAKAPSPETALRLPASGTHLAP 6958  
DB 1561 RHLLKGGYTAGALPGLRPLMEHRVLEPEABEECATLLAKAPSPETALRLPASGTHLAP 1620  
QY 6959 GHSLSLEHDSPTSPSPSACGEAQLPSAPSGGAPIRDMGHPOQSKLPSTGHPGTAQ 7018  
DB 1621 GHSLSLEHDSPTSPSPSACGEAQLPSAPSGGAPIRDMGHPOQSKLPSTGHPGTAQ 1690  
QY 7019 PRPSPDSWGQAPAFCHPKQASQEQCSHPHAPACPGSPFPGSCKEAPLVPSSPFL 7078  
DB 1681 PRPSPDSWGQAPAFCHPKQASQEQCSHPHAPACPGSPFPGSCKEAPLVPSSPFL 1740  
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DB 1741 GQOQAPPAPAKAPPLDLSKVGPGDLSLPGRPKPGCSPPGSAQSSQVSSLRVSSQV 1800  
QY 7139 GTEPGSLDAEGWTOEABDLSTSTLQRPQOATMRKFSLGRGQYAGVAGYGTAFPGG 7198  
DB 1801 GTEPGSLDAEGWTOEABDLSTSTLQRPQOATMRKFSLGRGQYAGVAGYGTAFPGG 1860  
QY 7199 DAGMGLGQPMWARIAWQSQEEBEEQBARAESQEQBARAESPLPOVSARPVPVVG 7258  
DB 1861 DAGMGLGQPMWARIAWQSQEEBEEQBARAESQEQBARAESPLPOVSARPVPVVG 1920  
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DB 2221 SSPCPDIDGEYADGVLLVMKPVESYGPVTYIYVQCSLEGGSWTTLASDIFDCCYLTSKLSR 2280  
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DB 2281 GGYTTRTACVSKAGMPYSSPEOVLGPGSHLASEESQGRSAQPLPSTKTFATQOI 2340  
QY 7679 QGRFVSVVRQCEWKAASGRALAAKIIIPYHPKDKTAVLRREYALKGLRHPLHQAALHAYLSP 7738  
DB 2341 QGRFVSVVRQCEWKAASGRALAAKIIIPYHPKDKTAVLRREYALKGLRHPLHQAALHAYLSP 2400  
QY 7739 RHLVLIILELCSGPELLPCLAEASYSSESEVKDYLWQNLATQYLNHOTHILHLDISENMI 7798  
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DB 2461 ITEYNILKVDLGNQAQSLSEKVLPSDKFKDYLETWAPLLELQOGAVPOTDIWAGVTAF 2520  
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DB 2521 IMLSAEYFVSSEGARDLQRLKGLVRLSRCYAGLSGGAVAFURSTLCAQPMGRPCASSC 2580  
QY 7919 LQCPWLTEGSPACSRPAPVTFTTARLURVVRNREXRALLYKRHNLAQVR 7968  
DB 2581 LQCPWLTEGSPACSRPAPVTFTTARLURVVRNREXRALLYKRHNLAQVR 2630

RESULT 5  
US-10-307-019-6  
; Sequence 6, Application US/10307019  
; Publication No. US20030108533A1  
; GENERAL INFORMATION:  
; APPLICANT: Zeng, Wenlin  
; APPLICANT: Stanton, Lawrence  
; APPLICANT: SCIOS, INC.  
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION  
; FILE REFERENCE: SCIOS.021DV1  
; CURRENT APPLICATION NUMBER: US/10/307,019  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/548,473  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/129,552  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 2596  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-307-019-6

Query Match 32.8%; Score 13528; DB 14; Length 2596;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2595; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MLERFPTKVKKGSSITFSVKVEGRPVPTVHMLREAEAGVLMIGDTPGYTVASSAQOH 60  
QY 5433 SLVLLDVGRHQGYTTCIASNAAGQALCSASLHVSGLPKVEEKEVKKEALISTFLOQTQ 5492  
DB 61 SLVLLDVGRHQGYTTCIASNAAGQALCSASLHVSGLPKVEEKEVKKEALISTFLOQTQ 120  
QY 5493 AISAQGLETFADLQGRKEEPLAAKEALHLSLAEVGTEEFLOKLTQITTEWMSAKIT 5552  
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DB 241 PLGAEQDAITLREGQYVEVLDAAHPURLWVTRPTKSPSRQGWVSPAYLDRRLKLSPEW 300  
QY 5673 GAEEAPFPCEAYSEDEYKARLSVVOELLSSQAFVEELOFQSHHLOHLERCPHVPIA 5732  
DB 301 GAEEAPFPCEAYSEDEYKARLSVVOELLSSQAFVEELOFQSHHLOHLERCPHVPIA 360  
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Db 1081 PDSEKQSHRRKLHGFYEVKEIGRGVGFVKRVQHKNGKILCAAKFIPLRSRTQAAYRE 1140  
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Db 1141 RDILAAALSHPVATGLDOFETKTLILILELCSSEHLLDRLYKGVVTEAEVKVYIQOAV 1200  
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QY 6633 EIIQONPVSEASDIWAMGVISYLSLTCSPPAGESDRAITLVLEGRVSWSSPMAHLSE 6692  
Db 1261 EIIQONPVSEASDIWAMGVISYLSLTCSPPAGESDRAITLVLEGRVSWSSPMAHLSE 1320  
QY 6693 DAKOFIKATLQAPQAPSAQCLSHPWFLKSMFAEAEHFIINTKQLKFLILARSWORSIM 6752  
Db 1321 DAKOFIKATLQAPQAPSAQCLSHPWFLKSMFAEAEHFIINTKQLKFLILARSWORSIM 1380  
QY 6753 SYKSTILNRSITPELLRGPPDPSILGVARHLCRDYDGGSSSSSSSDDELAPFAKSLPPS 6812  
Db 1381 SYKSTILNRSITPELLRGPPDPSILGVARHLCRDYDGGSSSSSSSDDELAPFAKSLPPS 1440  
QY 6813 PVTHSPLHPRGFLRPSASLPEEAERSESTEAPAPASPEGAGPAAQCVPRHVSIRS 6872  
Db 1441 PVTHSPLHPRGFLRPSASLPEEAERSESTEAPAPASPEGAGPAAQCVPRHVSIRS 1500  
QY 6873 LFYHQAGSPHGHALPGSRHPRARRHLLKGGYIAGALPGLREPLMEHRVLEBEAAREE 6932  
Db 1501 LFYHQAGSPHGHALPGSRHPRARRHLLKGGYIAGALPGLREPLMEHRVLEBEAAREE 1560  
QY 6933 QATILAKAPSPETALRUPASGTHLAPGSHSHLEHDSPTPRPSEACGEAQRUPSPAGG 6992  
Db 1561 QATILAKAPSPETALRUPASGTHLAPGSHSHLEHDSPTPRPSEACGEAQRUPSPAGG 1620  
QY 6993 APIRDMGHPOQSKQLPSTGCHPGTAQPRSPDPSFWQOPAPFCHPKQGSAPQEGCSHPHA 7052

Db 1621 APIRDMGHPOQSKQLPSTGCHPGTAQPRSPDPSFWQOPAPFCHPKQGSAPQEGCSHPHA 1680  
QY 7053 VAPCPGSPFPFGCKEAPLVPSPSFFLQGOQAPAPAKASPPDLDSKMGPGDISLPRPKPG 7112  
Db 1681 VAPCPGSPFPFGCKEAPLVPSPSFFLQGOQAPAPAKASPPDLDSKMGPGDISLPRPKPG 1740  
QY 7113 PCSSPGASQASSQSVSLRVGSSQVGTGPGSLDAEGHTQEAEDLSSTPTLQRPQEOA 7172  
Db 1741 PCSSPGASQASSQSVSLRVGSSQVGTGPGSLDAEGHTQEAEDLSSTPTLQRPQEOA 1800  
QY 7173 TMKRFSLGGRGVAGVAGYGTFAFGDAGGMLGQOPMMARIAMAVSQSEEEQEEARAE 7232  
Db 1801 TMKRFSLGGRGVAGVAGYGTFAFGDAGGMLGQOPMMARIAMAVSQSEEEQEEARAE 1860  
QY 7233 QSEEQEAEAESEPLPOVSARPVPEVGRAPTRSPPTPWEDIGQVSLVQIRLSDGDAEA 7292  
Db 1861 QSEEQEAEAESEPLPOVSARPVPEVGRAPTRSPPTPWEDIGQVSLVQIRLSDGDAEA 1920  
QY 7293 DTLSLDSISEVDPAYLNLSDLYDIKYLPEFEMIIRKVPKSAQPEPPSPMAEELAEFPPT 7352  
Db 1921 DTLSLDSISEVDPAYLNLSDLYDIKYLPEFEMIIRKVPKSAQPEPPSPMAEELAEFPPT 1980  
QY 7353 WMPFGLPHAGLEITESEEDVDALLAEAAVGRKRWSSPSRSLPHFGHLPDEPAEL 7412  
Db 1981 WMPFGLPHAGLEITESEEDVDALLAEAAVGRKRWSSPSRSLPHFGHLPDEPAEL 2040  
QY 7413 GLERVKASVEHISRLIKRPEGLEKGGPRKPGGLASFRLSGLKSWDRAPFTLRELSDE 7472  
Db 2041 GLERVKASVEHISRLIKRPEGLEKGGPRKPGGLASFRLSGLKSWDRAPFTLRELSDE 2100  
QY 7473 TVVLGQSVTLACQVSAQPAQAATWSKDGAPLSSSRSLVLSATLKNFOLLTILVVAEDLG 7532  
Db 2101 TVVLGQSVTLACQVSAQPAQAATWSKDGAPLSSSRSLVLSATLKNFOLLTILVVAEDLG 2160  
QY 7533 VYTCVSVALGTVTGVLKRAERPSPPCPDPIGEVYADGVLLVWKPVESYGFVTYIVQC 7592  
Db 2161 VYTCVSVALGTVTGVLKRAERPSPPCPDPIGEVYADGVLLVWKPVESYGFVTYIVQC 2220  
QY 7593 SLEGGSWTTLASDIFDCCYLTSKLSRGTYTTRTACVSKAGMGPYSSPSEQVLLGSPSHL 7652  
Db 2221 SLEGGSWTTLASDIFDCCYLTSKLSRGTYTTRTACVSKAGMGPYSSPSEQVLLGSPSHL 2280  
QY 7653 ASBEEQSGRSAQPLSTKTFAFQTOIQRFVSFVQCEKASGRALAAKIIYPHPKDKTA 7712  
Db 2281 ASBEEQSGRSAQPLSTKTFAFQTOIQRFVSFVQCEKASGRALAAKIIYPHPKDKTA 2340  
QY 7713 VLREYEAALKGRPHLAQHAAYLSRPHLVLIILELCSGPELLPCLAEARASYSESEVKYL 7772  
Db 2341 VLREYEAALKGRPHLAQHAAYLSRPHLVLIILELCSGPELLPCLAEARASYSESEVKYL 2400  
QY 7773 WQMLSATQYLHNQHILHLDRSENMIITEYNLLKVVDLGNACSLSOEKVLPDSKFKDYLE 7832  
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QY 7833 TMAPELLEGGGAVPOTDINAIGVTAFIMLSAEVPSSEGDARDLQRLKGLVLRSCYAG 7892  
Db 2461 TMAPELLEGGGAVPOTDINAIGVTAFIMLSAEVPSSEGDARDLQRLKGLVLRSCYAG 2520  
QY 7893 LSGGAVAFLESTLCAQFWGRPCASSCLOCPWLTEGPACSRPAVPTFTPTARLRFVVRNRE 7952  
Db 2521 LSGGAVAFLESTLCAQFWGRPCASSCLOCPWLTEGPACSRPAVPTFTPTARLRFVVRNRE 2580  
QY 7953 KRRALLYKRNHQAQVR 7968  
Db 2581 KRRALLYKRNHQAQVR 2596

RESULT 6  
US-10-093-463-72  
; Sequence 72, Application US/10093463  
; Publication NO. US20030208039A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigara, Muralidhara

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2004, 11:16:23 ; Search time 92 Seconds  
(without alignments)  
4471.258 Million cell updates/sec

Title: US-10-077-130-5  
Perfect score: 41273  
Sequence: 1 MDQPSGAPFLTRPKAFV.....RNREKRALLYKRNLAQVR 7968

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*
- 2: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*
- 3: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*
- 4: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*
- 5: /cgn2\_6/prodata/2/iaa/5A COMB.pep.\*
- 6: /cgn2\_6/prodata/2/iaa/5B COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8423	20.4	1665	4	US-09-858-664A-2
2	8423	20.4	1665	4	US-10-274-978-2
3	1173	2.8	846	4	US-09-858-664A-3
4	1173	2.8	846	4	US-10-274-978-4
5	909.5	2.2	549	4	US-09-858-664A-5
6	909.5	2.2	549	4	US-10-274-978-6
7	892.5	2.2	2860	2	US-08-826-267-2
8	592.5	1.4	414	4	US-09-858-664A-13
9	592.5	1.4	414	4	US-10-274-978-14
10	531	1.3	279	4	US-09-858-664A-4
11	531	1.3	279	4	US-10-274-978-5
12	521	1.3	298	4	US-09-858-664A-17
13	521	1.3	298	4	US-10-274-978-18
14	511.5	1.2	508	4	US-09-858-664A-18
15	511.5	1.2	508	4	US-10-274-978-19
16	504	1.2	250	4	US-09-858-664A-6
17	504	1.2	250	4	US-10-274-978-7
18	489	1.2	448	2	US-09-159-385-2
19	489	1.2	448	3	US-09-186-277-2
20	476.5	1.2	11877	3	US-09-105-537-6
21	472.5	1.1	260	2	US-07-857-224B-23
22	466.5	1.1	454	2	US-09-159-385-1
23	466.5	1.1	454	3	US-09-186-277-1
24	466	1.1	274	4	US-09-858-664A-14
25	466	1.1	274	4	US-10-274-978-15
26	465	1.1	358	4	US-09-230-896C-29
27	464.5	1.1	1050	4	US-09-428-711A-16

28	456	1.1	331	3	US-08-810-712-24	Sequence 24, Appl
29	456	1.1	1423	3	US-08-810-712-10	Sequence 10, Appl
30	454.5	1.1	356	4	US-09-733-388-4	Sequence 4, Appl
31	454	1.1	1651	3	US-09-540-245A-18	Sequence 18, Appl
32	451.5	1.1	1051	4	US-09-428-711A-14	Sequence 14, Appl
33	446	1.1	424	2	US-08-715-568A-1	Sequence 1, Appl
34	438.5	1.1	385	4	US-09-733-388-2	Sequence 10, Appl
35	436	1.1	355	4	US-09-579-664B-10	Sequence 10, Appl
36	433	1.0	261	2	US-07-857-224B-22	Sequence 22, Appl
37	432	1.0	343	2	US-08-878-989-5	Sequence 5, Appl
38	432	1.0	343	3	US-09-272-796-5	Sequence 5, Appl
39	427	1.0	370	2	US-08-878-989-19	Sequence 19, Appl
40	427	1.0	370	3	US-09-272-796-19	Sequence 19, Appl
41	427	1.0	370	4	US-09-457-040B-31	Sequence 31, Appl
42	418.5	1.0	1395	3	US-09-540-245A-15	Sequence 15, Appl
43	413.5	1.0	307	1	US-08-713-828-1	Sequence 1, Appl
44	413.5	1.0	307	2	US-08-919-627-1	Sequence 1, Appl
45	413.5	1.0	307	2	US-09-096-245-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-858-664A-2  
; Sequence 2, Application US/09858664A  
; Patent No. 6482624

; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui, et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; THEREOF

; FILE REFERENCE: CLO00927-CIP  
; CURRENT APPLICATION NUMBER: US/09/858,664A

; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 09/711,134

; PRIOR FILING DATE: 2000-11-11  
; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2

; LENGTH: 1665  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-09-858-664A-2

Query March 20.4%; Score 8423; DB 4; Length 1665;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 53 PPSMQVTIEDVQACTGCTAGTAEIIEGDPQPSVTWYKDSVQLVDSTRLSQOQEGTYSLV 112

QY 6416 LRHVASKDAGVYTCIAONTGGVLCXAEILLVGGDNEPSEKSHRRKHLHSFYEVKEEIG 6475

Db 113 LRHVASKDAGVYTCIAONTGGVLCXAEILLVGGDNEPSEKSHRRKHLHSFYEVKEEIG 172

QY 6476 RGVEFGVKRVQHKGNKILCAAKPIPLRSRTAQAAYRERDILAAALSHPLVTGLLDQFETRK 6535

Db 173 RGVEFGVKRVQHKGNKILCAAKPIPLRSRTAQAAYRERDILAAALSHPLVTGLLDQFETRK 232

QY 6536 TLILILECSSEELLRLRYKGVVTEAEVKVYIQQLVEGLVHSHGVHLHDKPSNIML 6595

Db 233 TLILILECSSEELLRLRYKGVVTEAEVKVYIQQLVEGLVHSHGVHLHDKPSNIML 292

QY 6596 VHPAREDIKICDFGAQNTTPAELOFSQVSGSPFVSPETIIQONPVSFASDIWAGVISYL 6655

Db 293 VHPAREDIKICDFGAQNTTPAELOFSQVSGSPFVSPETIIQONPVSFASDIWAGVISYL 352

QY 6656 SLTCCSPFAGESDRATLLNVLGRVSWSPMAHLSEDAKDFIKATLQAPQARPSAQC 6715

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Db 1553 TAFIMLSAEYPVSSBGARDLQGLRKGLVRLSRCYAGLSGGAVAFLESTLCAQPWGRPCA 1612

QY 7916 SSCLOCPMLTTEGPACSRPAVTFPTFARLVFVRNREKERALLYKEHNLAQVR 7968

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RESULT 2

US-10-274-978-2

; Sequence 2, Application US/10274978

; Patent No. 6670184

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui, et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL000927-CIP-DIV

; CURRENT APPLICATION NUMBER: US/10/274,978

; CURRENT FILING DATE: 2002-10-22

; PRIOR APPLICATION NUMBER: 09/859,664

; PRIOR FILING DATE: 2001-05-17

; PRIOR APPLICATION NUMBER: 09/711,134

; PRIOR FILING DATE: 2000-11-14

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1665

; TYPE: PRT

; ORGANISM: Human

US-10-274-978-2

Query Match 29.4%; Score 8423; DB 4; Length 1665;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 6476 RGVFGFVQVQHGKNILCAAKFIPLRSRTRAQAVRERDILAAISHPLVTGLLDQPETRK 6535

Db 173 RGVFGFVQVQHGKNILCAAKFIPLRSRTRAQAVRERDILAAISHPLVTGLLDQPETRK 232

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QY 6596 VHPAREDIKIDFGFAQNTIPAELOFSQGSPEFVSPEIIQONPVSEASDIWAMGVISYL 6655

Db 293 VHPAREDIKIDFGFAQNTIPAELOFSQGSPEFVSPEIIQONPVSEASDIWAMGVISYL 352

QY 6656 SITCSSPAGESDRATLLNVLEGRVSWSSPMAHLSEDADKFTKATQAPQARPSAAQC 6715

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Db 413 LSHPWFLKSMPAEAAHFINTKQLKELLARSVQRSLMSYKSIIVWRSIPELLRGPDSPS 472

QY 6776 LGVASHLCRDTCGSSSSSSSSSNEELAPPARAKSLPPSVTHSPLLPGRGLRPSASIPER 6835

Db 473 LGVASHLCRDTCGSSSSSSSSSNEELAPPARAKSLPPSVTHSPLLPGRGLRPSASIPER 532

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